



Evolution and Preference for Local Risk


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Evolution and Preference for Local Risk*

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Abstract

Our understanding of risk preferences can be sharpened by considering their evolutionary basis. Recently, [Robatto & Szentes \(2017\)](#) found that both aggregate risk and idiosyncratic risk generate the same growth rate in a continuous time setting. We introduce a new source of risk, which is correlated between agents in the same location, but is uncorrelated between agents in different locations. We show that this local risk induces a strictly higher growth rate. This shows that interdependence of risk and population structure have important implications in a continuous-time setting, and that natural selection induces individuals to prefer local risk.

JEL Classification: D81, D91. **Keywords:** Risk preferences, evolution, risk interdependence, long-run growth rate.

1 Introduction

Our understanding of preferences can be sharpened by considering their evolutionary basis (see [Robson & Samuelson, 2011](#) for a survey). One intriguing result from this literature ([Robson, 1996](#); see also [Lewontin & Cohen, 1969](#); [McNamara, 1995](#)) is that idiosyncratic (independent) risk induces a higher long-run population growth rate than aggregate (correlated) risk. This

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implies that natural selection should favor agents who prefer idiosyncratic risk to aggregate risk.¹

Robson’s (1996) model is based on discrete time, in which the basic time period is a single generation. Recently, Robatto & Szentes (2017) cast a surprising light on this result. Specifically, they recast Robson’s model in a continuous-time setting (which, arguably, may better fit human population dynamics), and show that both risks induce the same long-run growth rate. Thus, Robatto & Szentes’s result suggests that natural selection should induce agents to ignore interdependence of risk, and to always choose the alternative with the highest expected growth rate.²

In this paper, we show that interdependence of risk has important implications on the long-run growth rate even in a continuous-time setting. Specifically, we introduce a new source of risk, called local risk, that is correlated between agents who live in the same location, but is uncorrelated between agents in different locations. We show that this local risk induces a strictly higher growth rate than either idiosyncratic risk or aggregate risk.

The intuition is that the impact of risk interdependence on the growth rate depends on the “direction” of the interdependence (vertical or horizontal). Local risk induces correlation between an agent’s outcome and her offspring’s outcome (as they, initially, share the same location). This vertical correlation is helpful to the growth rate, as it allows successful families to have fast exponential growth. By contrast, local risk minimizes horizontal correlation of risk between agents of the same cohort. This horizontal correlation is harmful to the growth rate as periods in which all agents have a low growth rate have a large negative influence on the long-run growth rate.

We offer two main interpretations of the locations in our model. First, they may represent geographical locations of prehistoric bands. An individual is born in her parent’s band, and individuals may occasionally leave their band and join (or start) a new band. Second, one can interpret location in a broader sense as any heritable trait that influences the birth rate, where the trait may be inherited either through biological processes or through learning from the parent. One example of such a trait is hunting technique in a hunter-gatherer society, where an individual is likely to adopt her parent’s technique, and there is a higher correlation between the outcomes of those who use the same technique.

¹See Heller (2014) for a discussion of why this may induce agents to be overconfident in the sense of overestimating the accuracy of their private information.

²We focus on Robatto & Szentes’s (2017) result on continuous environmental variations, where aggregate risk induces the same long-run growth rate as idiosyncratic risk. Robatto & Szentes also study sudden natural disasters, and show that in such settings natural selection favors agents who are averse to aggregate risk associated with natural disasters. As Robatto & Szentes (2017, p. 418) summarize in: “That is, conditional on the risk associated with natural disasters, choices will be based only on the expected rate of reproduction. It is irrelevant whether environmental variations are aggregate or idiosyncratic.” Further discussion of this issue (and of what should be regarded as the “expected rate of reproduction”) is presented in Section 6.

Our key result is that agents should prefer local risk. That is, an agent should prefer sharing risk with her parent, while diversifying risk with respect to the rest of the population. We think that the insight that vertical risk correlation increases the growth rate, while horizontal risk correlation decreases the growth rate, may be interesting in other domains of economics and finance, such as in capital allocation problems.³

The way in which idiosyncratic risk has been modeled in the existing literature captures well coin flips that have only immediate effects. However, it is compelling that the growth rate in the evolutionary past was partly determined by risk with effects that persist from parents to offspring. We show that this inherited idiosyncratic risk induces a higher growth rate than aggregate risk, and natural selection should induce people to prefer this form of idiosyncratic risk to aggregate risk. Such inherited idiosyncratic risk is discussed in Remark 1.

2 Informal Treatment of Key Result

The following example conveys the gist of Robson’s (1996) argument that individuals should be more averse to aggregate risk than to comparable idiosyncratic risk. Suppose that there is discrete time and the age structure is trivial in that individuals are born, live one period, have offspring (with asexual reproduction), and die before the next period.

Consider the following evolutionary race between two types. Type I has two offspring with probability $1/2$, or one offspring also with probability $1/2$. Risk here is idiosyncratic. Type II also has two offspring with probability $1/2$, or one with probability $1/2$, but now the risk is aggregate. By applying the exact law of large numbers to an infinite population, the number of agents of type I at time T is $y(T) = (3/2)^T$ (normalizing $y(0) = 1$), so that the growth rate is equal to $\frac{1}{T} \cdot \ln y(T) = \ln(3/2)$. The number of agents of type II is $z(T) = 2^{n(T)}$ (normalizing $z(0) = 1$), where $n(T)$ is the number of heads in a sequence of T flips of a fair coin. Hence $\frac{1}{T} \cdot \ln z(T) = \frac{n(T)}{T} \ln 2 \rightarrow \frac{1}{2} \ln 2 = \ln \sqrt{2} < \ln(3/2)$, w.p. 1, by the strong law of large numbers. It follows that $\frac{z(T)}{y(T)} \rightarrow_{T \rightarrow \infty} 0$, w.p. 1. The type undergoing aggregate risk is strictly disadvantaged relative to the type undergoing idiosyncratic risk with precisely the same distribution. Furthermore, note that $\frac{1}{T} \cdot \ln E(z(T)) = \ln(3/2)$. That is, $z(T)$ is “swamped” by its own mean.

The following example shows how embedding this issue in continuous time may lead to different results, as argued by Robatto & Szentes (2017). Suppose that there is a single unstructured population in which the fertility rate is independent of the agent’s age. For simplicity, we focus on fertility, so that there is no mortality. Both types induce the same marginal distribution

³The advantage of vertical risk correlation has been coined the *multiplayer effect* by McNamara & Dall (2011). The disadvantage of horizontal risk correlation is called *within-generation bet hedging* (see, e.g., Lehmann & Balloux, 2007, and the citations therein). Both effects have been studied in the biological evolutionary literature, mostly in setups of non-overlapping generations and lotteries over the number of offspring.

over annual fertility rates: r_h with probability 50% and r_l with probability 50%. Type I induces idiosyncratic risk. Applying the law of large numbers, the number of agents of type I at time t is equal to $y(t) = e^{0.5 \cdot (r_h + r_l) \cdot t}$, and the annual growth rate is equal to $\frac{1}{t} \cdot \ln y(t) = 0.5 \cdot (r_h + r_l) \equiv \mu$.

Type II induces aggregate risk. There are two states: h and l . In state h , all agents have fertility rate r_h , and in state l , all agents have fertility rate r_l . There is a continuous probability rate λ that the state is redrawn. If it is, the fertility rate is r_h with probability 50% and r_l with probability 50%. What is the growth rate of the population exposed to this aggregate risk? If $z(t)$ is the population at time t , it follows that

$$\frac{\ln z(t)}{t} = \frac{r_h \cdot (\text{time in state 1}) + r_l \cdot (\text{time in state 2})}{t} \xrightarrow{t \rightarrow \infty} 0.5 \cdot (r_h + r_l) = \mu,$$

as a consequence of the evident ergodicity of the process. Thus, both idiosyncratic risk and aggregate risk induce the same growth rate.

A simplified version of our key result, then is as follows. Suppose that there is an infinite number of subpopulations, each with an infinite number of members. There are two possible birth rates r_h and r_l , where $r_h > r_l$. At $t = 0$, a draw is made so that these rates have equal probabilities. The death rate remains zero. These draws for the birth rates are independent across subpopulations, so that half of each subpopulation gets r_h and the remaining half gets r_l . Furthermore, an independent redraw from this distribution for each subpopulation is held throughout the process at a constant Poisson rate of $\lambda > 0$. Each subpopulation grows at rate $\mu = 0.5 \cdot (r_h + r_l)$. However, the overall population grows faster than all of its identical isolated subpopulations. Indeed, suppose that the growth rate of the overall population is $g(\lambda)$. Then we show that $g(\lambda)$ is decreasing in λ , $g(\lambda) \rightarrow \mu$ as $\lambda \rightarrow \infty$, and $g(\lambda) \rightarrow r_h > \mu$ as $\lambda \rightarrow 0$.

How can the overall population grow faster than all of its identical subpopulations? The normalized size of the overall population must be the mean of the size of each subpopulation, given the statistical independence. Hence the mean must grow faster than the subpopulations.

Note the relationship to the example from [Robson \(1996\)](#) discussed above, where $z(T)$ grows at limiting rate $\ln(\sqrt{2})$ but its mean, $E(z(T))$, grows faster, at rate $\ln(3/2)$. With an infinite number of subpopulations, each with its own local shock, the overall population would be governed by the law of large numbers, and so would grow at rate $\ln(3/2)$.

To get an intuition for this key result, consider this simplification. The local shocks are still drawn independently, but these redraws arrive deterministically and in synchrony every τ periods, which is comparable to an arrival rate of $\lambda = 1/\tau$. On each draw, half of the subpopulations get r_h and the remaining half get r_l .

If the initial population is of size 1, then, after a time $k \cdot \tau$ the population is $N(k \cdot \tau) =$

$(0.5 \cdot (e^{r_h \cdot \tau} + e^{r_l \cdot \tau}))^k$, so that

$$\frac{1}{k \cdot \tau} \ln N(k \cdot \tau) = \frac{1}{\tau} \cdot \ln(0.5 \cdot (e^{r_h \cdot \tau} + e^{r_l \cdot \tau})) = \bar{g}(\lambda).$$

It follows that $\bar{g}(\lambda) \rightarrow r_h$ and $\bar{g}(\lambda) \rightarrow \mu = 0.5 \cdot (r_h + r_l)$, if $\tau \rightarrow \infty$ or $\lambda \rightarrow 0$. We will show that the simplification that redraws occur at deterministic intervals is harmless.

Remark 1 (Inherited idiosyncratic risk). Suppose that all of the risk is idiosyncratic so that redraws occur independently for every agent with arrival rate λ . At each redraw, the agent gets a fertility rate r_h or r_l with equal probabilities. The existence of subpopulations is then irrelevant. Suppose, however, that offspring do not get a fresh draw but inherit the realization of the parent. Such a population grows at the rate $g(\lambda)$ as before. To get an intuition for why this is true, consider again the simplification that all redraws arise in synchrony at deterministic intervals. At each of these draws, half of the *population* gets rate r_h and half gets r_l . It follows that, after a time $k\tau$, the population is still $N(k\tau) = (0.5 \cdot e^{r_h \cdot \tau} + 0.5 \cdot e^{r_l \cdot \tau})^k$; thus the population grows at the same rate $\bar{g}(\lambda)$ as before and the above observations apply.

What this highlights is that the previous literature makes an implicit assumption that each offspring is given a fresh draw. It follows that the growth rate of the population is simply $\mu = 0.5 \cdot (r_h + r_l)$, independently of λ . For the expected fertility rate to be a valid evolutionary criterion, offspring must be undifferentiated, which is the case if each offspring is given a fresh draw. If offspring instead inherit the choice of their parents, then the composition of the population matters. If each offspring inherits her mother's fertility rate, the present analysis shows that the overall growth rate in a single population is higher with this inherited idiosyncratic risk than with aggregate risk, since $g(\lambda) > \mu$, in contrast to [Robatto & Szentes \(2017\)](#). The results of the present paper show that local risk is equivalent to inherited idiosyncratic risk.

3 Model

Consider a continuum population of an initial mass one. Time is continuous, indexed by $t \in \mathbb{R}^+$, and measured in years. The environment includes a continuum of different locations. Initially, each agent is located in a different location.

In what follows we define a random *growth process* that depends on the parameters $(\delta, (\{x_l, x_h\}, q, \lambda_r, \lambda_m), (Y, q_y, \lambda_y), (Z, q_z, \lambda_z))$, which are described below.

To simplify the model, we assume that there is a constant *death rate* $\delta \geq 0$ for each agent. Reproduction is asexual. The parameter $\mathbf{b}^i(t)$ is the (total) birth rate of each individual i at time t . It is the sum of three random variables $\mathbf{b}^i(t) = \mathbf{x}^i(t) + \mathbf{y}^i(t) + \mathbf{z}(t)$. We describe each in turn.

1. The *local birth rate*, $\mathbf{x}^i(t) \geq 0$, is a random variable that describes the local component of the birth rate (henceforth, *local birth rate*). The local birth rate is aggregate in that it is the same for all agents in the same subpopulation, while it is independent of the birth rate of agents in other subpopulations. To simplify the analysis we assume that the random variable $\mathbf{x}^i(t)$ has two possible values, namely $\text{supp}(\mathbf{x}^i(t)) = \{x_l, x_h\}$, where $0 \leq x_l < x_h$, and the probability of x_h is $q \in (0, 1)$. A numerical analysis suggests that the results remain similar for an arbitrary support of $\mathbf{x}^i(t)$.
2. The *idiosyncratic birth rate*, $\mathbf{y}^i(t) \geq 0$, is a random variable that describes the idiosyncratic component of the birth rate. The idiosyncratic birth rate is independent of the corresponding component of the birth rate of any other agent in the population. We assume that the random variable \mathbf{y}^i has a finite support $Y = \text{supp}(\mathbf{y}) = \{y_1, \dots, y_{n_y}\}$.
3. The *aggregate birth rate*, $\mathbf{z}(t) \geq 0$, is a random variable that describes the aggregate component of the birth rate. All agents in the population share the same aggregate birth rate. We assume that the random variable \mathbf{z}^i has a finite support $Z = \text{supp}(\mathbf{z}(t)) = \{z_1, \dots, z_{n_z}\}$.

In our analysis we apply the exact law of large numbers. For example, we assume that the share of agents having an initial local high birth rate x_h is exactly⁴ q .

At time $t = 0$ the aggregate birth rate ($\mathbf{z}(0)$) is randomly determined according to the distribution q_z , and the idiosyncratic birth rate $\mathbf{y}^i(0)$ is randomly determined for each agent i according to the distribution q_y independently of all other random variables. In each subpopulation, the initial local birth rate is equal to x_h with probability $q \in (0, 1)$ and is equal to x_l with the remaining probability of $1 - q$ (independently of all other random variables).

The values of the different components of the birth rate evolve according to Poisson processes. Specifically, in each brief period of time Δ , the aggregate birth rate and the local birth rate further evolve as follows:

1. A new random value of the aggregate birth rate is drawn independently (according to q_z) with a probability of $\lambda_z \cdot \Delta$, where $\lambda_z > 0$ is the annual frequency with which the aggregate birth rate changes. This aggregate birth rate applies to all individuals in the entire population equally.
2. A new random value of the local birth rate of each location is drawn independently (to be x_h with probability q and x_l with probability $1 - q$) with a probability of $\lambda_r \cdot \Delta$, where

⁴The formalization of the intuitive claim that the independent probability of each agent obtaining a realized idiosyncratic birth rate of x_k is equal to the fraction of agents obtaining a realized idiosyncratic birth rate of x_k raises various technical difficulties. We refer the interested reader to [Duffie & Sun \(2012\)](#) (and the citations therein) for details on how the above intuitive claim of the exact law of large numbers can be formalized in a related setup.

$\lambda_r > 0$ is the frequency with which the local birth rate of each location changes. This local birth rate applies to all members of the same subpopulation.

The random events of death, birth, and migration are determined for each agent according to independent Poisson processes. Given the aggregate birth rate and local birth rate, in each brief period of time between t and $t + \Delta$, each agent i in the population:

1. Dies with a probability $\delta \cdot \Delta$.
2. Produces an offspring with probability $\mathbf{b}^i(t) \cdot \Delta$; the new offspring j shares the same local birth rate as her mother i (i.e., $x^j(t) = x^i(t)$); by contrast, the offspring takes a new independent draw to determine the value of the idiosyncratic birth rate y^j according to distribution q_y .
3. Draws a new value of the idiosyncratic birth rate (according to distribution q_y) with a probability of $\lambda_y \cdot \Delta$, where $\lambda_y > 0$ is the annual rate at which the idiosyncratic birth rate of each agent switches.
4. Changes location with a probability of $\lambda_m \cdot \Delta$, where $\lambda_m > 0$ is interpreted as the rate at which each agent changes location (migrates). The migrating agent draws a new value of the local birth rate (x_h with probability q and x_l otherwise).

Each of the above random variables is independent of the other random variables. In particular, the event that an agent changes location is independent of the event that her offspring (or her parent) migrates. That is, initially, an offspring and a parent share the same local birth rate, but their local birth rates become independent as soon as one of them randomly migrates.

4 Key Result

Let $\mathbf{w}(t)$ denote the mass of the population at time t . We normalize $\mathbf{w}(0) = 1$. We say that the growth process of $\mathbf{w}(t)$ given by $(\delta, (x_l, x_h, q, \lambda_r, \lambda_m), (Y, q_y, \lambda_y), (Z, q_z, \lambda_z))$ has an *equivalent (long-run) growth rate* $g \in \mathbb{R}$ if and only if

$$\lim_{t \rightarrow \infty} \frac{\ln \mathbf{w}(t)}{t} = g, \text{ almost surely.}$$

Let $\mu_x = q \cdot x_h + (1 - q) \cdot x_l$ (resp., $\mu_y = \sum y_k \cdot q(y_k)$, $\mu_z = \sum z_k \cdot q(z_k)$) be the expectation of the local (resp., idiosyncratic, aggregate) birth rate. Let $\lambda_x = \lambda_m + \lambda_r$ be the total rate at which an agent changes her local birth rate, either due to the agent changing location or due to the agent's location redrawing its local birth rate.

We show that the equivalent growth rate is the sum of four components: $g = f(x_l, x_h, q, \lambda_x) + \mu_y + \mu_z - \delta$. The novel part of the result concerns the component that depends on the local birth rate. In particular, we show that the function $f(x_l, x_h, q, \lambda_x)$ is decreasing in λ_x , such that the more persistent the local birth rate is, the higher the long-run growth rate. In the limit, $\lim_{\lambda_x \rightarrow 0} f(x_l, x_h, q, \lambda_x) = x_h$. That is, the local component of the growth rate is equal to the high realization x_h . Only with a highly transient local birth process does this component contribute its expectation to the total birth rate, i.e., $\lim_{\lambda_x \rightarrow \infty} f(x_l, x_h, q, \lambda_x) = \mu_x$.

The results on the idiosyncratic and aggregate components of the overall growth rate accord with [Robatto & Szentes \(2017\)](#), namely, these components are equal to μ_y and μ_z , respectively. By contrast, the local growth component is generally greater than μ_x . The share of agents having a high growth rate converges to a higher value than q . This is because, at each point in time, agents with a high local birth rate tend to have more offspring and these offspring share the parent's local birth rate. Hence, in a steady state, the share of agents with a high local birth rate is strictly higher than q .

More formally,

Theorem 1. *Let $(\delta, (x_l, x_h, q, \lambda_r, \lambda_m), (Y, q_y, \lambda_y), (Z, q_z, \lambda_z))$ be a growth process. Then its equivalent growth rate is equal to:*

$$g = f(x_l, x_h, q, \lambda_x) + \mu_y + \mu_z - \delta,$$

where $f(x_l, x_h, q, \lambda_x)$ has the following properties: (1) $f(x_l, x_h, q, \lambda_x)$ is decreasing in λ_x , (2) $\lim_{\lambda_x \rightarrow 0} f(x_l, x_h, q, \lambda_x) = x_h$, and (3) $\lim_{\lambda_x \rightarrow \infty} f(x_l, x_h, q, \lambda_x) = \mu_x$.

Sketch of proof. Since the novel result here concerns local risk, let us suppose, for simplicity, that there is no aggregate risk, idiosyncratic risk, or mortality.⁵ Suppose further that the size of the population at time t is $w(t)$ and that a fraction p of this population has birth rate⁶ x_h . The net increase in each small interval Δt of those agents with birth rate x_h is then $p \cdot x_h \cdot w(t) \cdot \Delta t$ (offspring born to parents with a high birth rate who inherit this rate) minus $(p - q) \cdot \lambda_x \cdot w(t) \cdot \Delta t$ ($\lambda_x \cdot w(t) \cdot \Delta t$ agents have redrawn a fresh value for the local birth rate, and the share of x_h -agents among them has decreased from p to q). The net increase in the total number of agents is $p \cdot x_h \cdot w(t) \cdot \Delta t$ (offspring born to parents with a high birth rate) plus $(1 - p) \cdot x_l \cdot w(t) \cdot \Delta t$ (offspring born to parents with a low birth rate).

Intuitively, the equilibrium value of p should match the ratio of the net increase of agents

⁵The formal proof in the appendix considers the general case.

⁶The evolution of this overall fraction can be described without reference to the subpopulations, which implies that the argument applies equally well to inherited idiosyncratic risk (where each offspring inherits the parent's birth rate), as discussed in Remark 1.

with a high local birth rate to the net increase of the population, such that

$$p = \frac{(p \cdot x_h + (q - p) \cdot \lambda_x) \cdot w(t) \cdot \Delta t}{(p \cdot x_h + (1 - p) \cdot x_l) \cdot w(t) \cdot \Delta t} = \frac{p \cdot x_h + (q - p) \cdot \lambda_x}{p \cdot (x_h - x_l) + x_l}.$$

$$\Leftrightarrow p^2 \cdot (x_h - x_l) + p \cdot (\lambda_x - (x_h - x_l)) - q \cdot \lambda_x = 0.$$

Let $\Delta x = x_h - x_l$. This quadratic equation has a unique solution in the interval $[0, 1]$:

$$p(\lambda_x) = \frac{\Delta x - \lambda_x + \sqrt{(\Delta x - \lambda_x)^2 + 4 \cdot q \cdot \Delta x \cdot \lambda_x}}{2 \cdot \Delta x}.$$

It is easy to see that $\lim_{\lambda_x \rightarrow \infty} p(\lambda_x) = q$, and $\lim_{\lambda_x \rightarrow 0} p(\lambda_x) = 1$, and so the stated results follow. The appendix shows further that $p(\lambda_x)$ is decreasing in λ_x , and that any initial value of p adjusts according to the net inflows of agents with each value of x , such that the induced differential equation for p is globally stable, which implies that $p \rightarrow p(\lambda_x)$ as $t \rightarrow \infty$. \square

5 Numerical Analysis of Finite Populations

Our analysis concerns a continuum population. How well does a continuum population approximates a finite population with a large number of subpopulations, each with a large number of members? A sharper question is: Suppose that there is no migration, no aggregate or idiosyncratic component of growth, but only constant idiosyncratic mortality. Suppose, further, that the growth rate predicted by the continuum model for the overall population is positive, but the growth rate predicted as in [Robatto & Szentes \(2017\)](#) for each subpopulation is negative. How does this tension play out? How can both results be valid?

As is inevitable, since each subpopulation is doomed to extinction, so too is the overall finite population. However, the fact that the continuum model rate derived here is positive, or that the mean size of each subpopulation grows, implies that the overall population may grow significantly in the interim. As the finite model converges to the continuum model, this initial growth phase becomes more and more prolonged, and the inevitable ultimate demise of the population is postponed indefinitely.

When there is no migration, a large structured population tends to ultimately put all its eggs in one basket. That is, the distribution of the finite population over its subpopulations tends to become very unequal, often concentrated in just one subpopulation. Such large subpopulations hold up the mean—the growth rate found here. Once the population is concentrated like this, however, doom is inevitable because the local risk of a large subpopulation, essentially, becomes aggregate since it affects a large share of the entire population.

Migration introduces a new element to these observations. Recall that, in the continuum

model, the migration rate is equivalent to the rate at which the local growth process is redrawn. Indeed, migration is an alternative way that an individual local growth process is reset. In the finite model, however, migration has a distinct effect from that of the redraw rate. If some subpopulations grow large, and others shrink, migration acts to redistribute the population. This means that the population can exploit the numbers in the large subpopulations, while diversifying the risk. These observations motivate the simulations described below.

5.1 Brief Description of the Simulations

The simulations model a finite population of agents that are randomly assigned to a finite set of locations in period zero.⁷ In period zero each agent is randomly endowed with an idiosyncratic birth rate, each location is randomly endowed with a local birth rate, and the world is endowed with a random aggregate birth rate (where each distribution has arbitrary finite support). Time is discrete. In the simulation runs described below we chose the length of each period to be one year.

In each period, each agent may experience three random events:

1. Each agent has an offspring with the probability induced by the agent's total birth rate. The new agent is born in the same location as the parent.
2. Each agent migrates to a random location with a probability of λ_m .
3. Each agent dies with the probability δ induced by the fixed death rate.

In addition, each location is endowed with a new random local birth rate with a probability of λ_r , and the world is endowed with a new random aggregate birth rate with a probability of λ_z .

5.2 Numerical Results

We describe here the results of 150=15·10 simulation runs. In each simulation run, the initial population includes 3,000 agents that are initially randomly allocated to 300 locations. The aggregate birth rate and the idiosyncratic birth rate are both equal to zero (i.e., $\mu_y = \mu_z = 0$). The local birth rate in each location is randomly chosen to be either $x_l = 0\%$ or $x_h = 2\%$ with equal probabilities (i.e., $q = 0.5$). We set the annual rate at which a subpopulation switches the local birth rate to be $\lambda_x = \lambda_m + \lambda_r = 2\%$. We set the annual death rate at 1.4%, which implies that Theorem 1's prediction for a continuum population is that: (1) the share of agents with a high local birth rate converges to about 71%, and (2) the annual long-run growth rate will be

⁷The numerical analysis is based on a Python simulation that was kindly contributed to us by Renana Heller (the simulation code is included in the supplementary material).

about 0.014%. A naive prediction that treats local risk as if it were aggregate risk predicts a long-run growth rate of -0.4%. Each simulation run stops after either (1) the population size decreases below 10 (extinction), (2) the population size increases above 1,000,000, or (3) 20,000 years have passed.⁸

The various simulation runs study 11 different ratios $\frac{\lambda_m}{\lambda_r}$ of the migration rate relative to the local risk redrawing rate (while maintaining $\lambda_m + \lambda_r = 2\%$): 0.01, 0.02, 0.05, 0.1, 0.25, 0.5, 1, 2, 4, 10. Figure 1 presents 4 representative simulation runs with ratios: 0.01 ($\lambda_m = 0.02\%$, $\lambda_r = 1.98\%$), 0.05 ($\lambda_m = 0.1\%$, $\lambda_r = 1.9\%$), 0.25 ($\lambda_m = 0.4\%$, $\lambda_r = 1.6\%$), and 1 ($\lambda_m = \lambda_r = 1\%$).

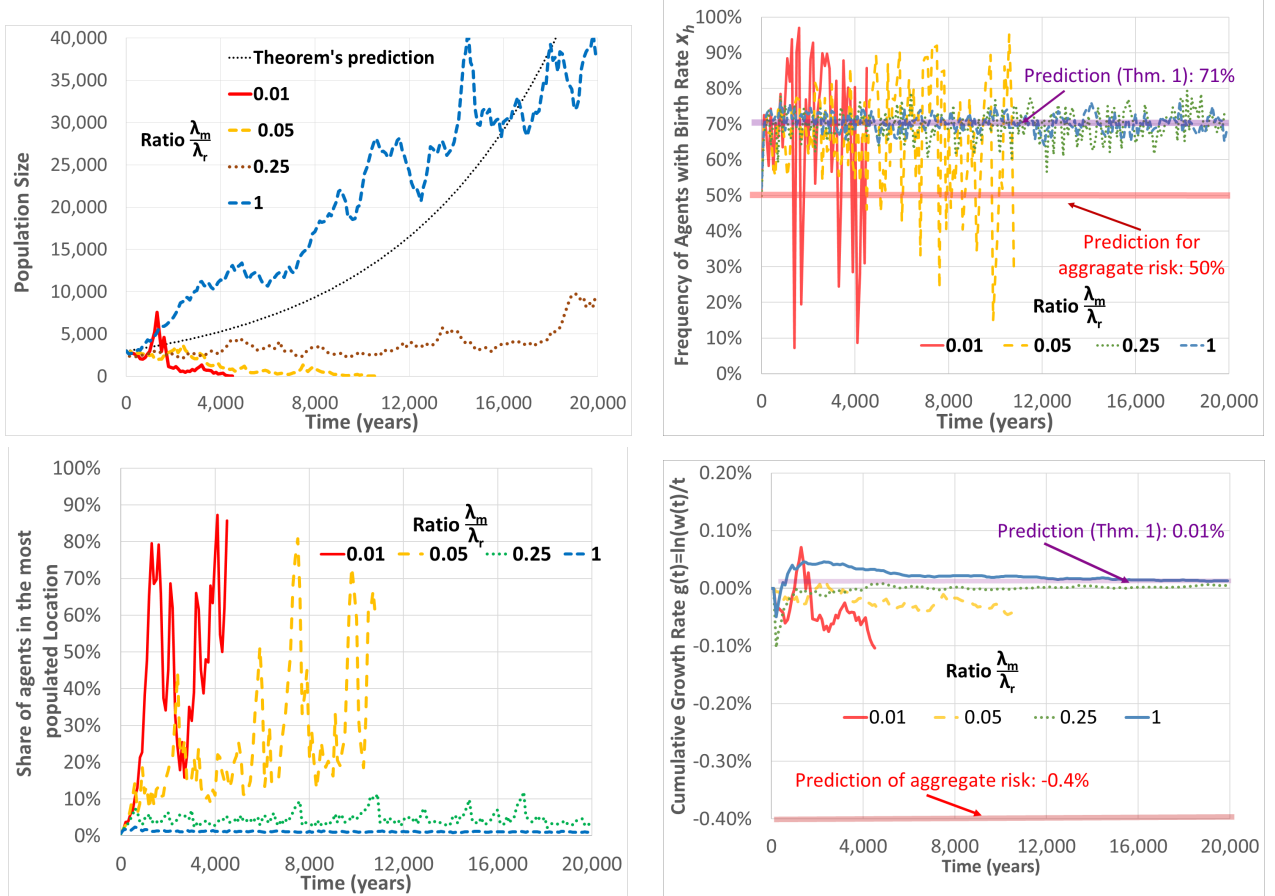


Figure 1: Representative Simulation Runs for four Ratios of $\frac{\lambda_m}{\lambda_r}$

The top-left panel of Figure 1 shows the dynamics of the total population in each of the four simulation runs. The top-right panel shows how the frequency of agents that are endowed with a high local birth rate evolves. The bottom-left panel shows the percentage of agents that live in the most populated location (among the 300 locations). The bottom-right panel shows the

⁸We stop the simulation run when the population size is below 10 (rather than waiting till the size is zero) in order to prevent error messages that occur when there are no agents at all. We stop the simulation run when the population size is above 1,000,000, since the simulation becomes very slow.

cumulative growth rate up to time t in each year (i.e., it shows $g(t) = \frac{\ln(w(t))}{t}$).

The figure shows that when the ratio $\frac{\lambda_m}{\lambda_r}$ is small (0.01 or 0.05), local risk has similar properties to aggregate risk. The low rate of immigration implies that a couple of “successful” locations (which happen to have had a high local birth rate for a long time) concentrate most of the population. This causes the local risk, essentially, to be aggregate. The frequency of agents with a high local birth rate has large fluctuations, since a single change of the local birth rate of the most populated location has a large impact on this frequency. This is shown in the top-right panel. The cumulative growth rate (bottom-right panel) is initially positive, but after a couple of thousand years it becomes negative and starts converging to the negative growth predicted by aggregate risk, until the population becomes extinct (top-left panel).

By contrast, the figure shows that when the ratio $\frac{\lambda_m}{\lambda_r}$ is 0.25 (resp., 1), then the predictions of Theorem 1 become relatively (resp., very) accurate for the finite population. When the immigration rate is sufficiently high, a “successful” location spreads its offspring to many other locations, staving off extinction. The bottom-left panel shows that the frequency of agents living in the most populated location is at most 10% (resp., 2%). This implies that the share of agents with a high local birth rate has a relatively (resp., very) small fluctuations around Theorem 1’s predicted value of about 71%, as can be seen in the top-right panel. The cumulative growth rate (bottom-right panel) converges to the positive value of 0.01%, as predicted in Theorem 1, as is shown in the top-left panel.

Figure 2 presents the mean long-run growth rate (and an interval of one standard deviation in each direction) obtained in the 15 simulation runs for each of the ten ratios of $\frac{\lambda_m}{\lambda_r}$. The results show that when the ratio is 0.1 or smaller, then the mean growth rate is substantially less than its predicted value of 0.014%, and the population usually becomes extinct. The ratio of $\frac{\lambda_m}{\lambda_r} = 0.25$ is borderline: the mean growth rate (0.005%) is relatively close to what Theorem 1’s predicts, and the population becomes extinct only in a single simulation run. When the ratio of $\frac{\lambda_m}{\lambda_r}$ is at least 0.5, Theorem 1 yields an excellent prediction: the mean growth rate is very close to 0.014%, and the population does not become extinct in any simulation run.

6 Discussion

Age structure Recently, a different approach was applied by Robson & Samuelson (2019) to show that risk interdependence matters in a continuous-time setting (see also related results in Robson & Samuelson, 2009). Specifically, they show that adding age structure to Robatto & Szentes’s (2017) setting (i.e., allowing the fertility rate to depend on the agent’s age) implies that interdependence of risk influences the growth rate. By contrast, the present paper shows that interdependence of risk is important for the induced growth rate in a hierarchical population,

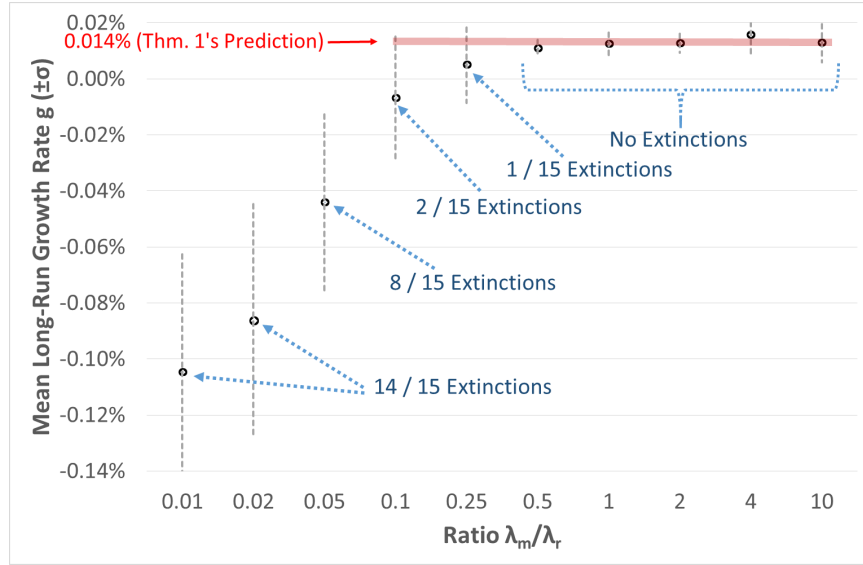


Figure 2: Mean Long-Run Growth Rate for each Ratio of $\frac{\lambda_m}{\lambda_r}$

The black points describe the mean growth rate of 15 simulation runs for each ratio of $\frac{\lambda_m}{\lambda_r}$. The gray bars show intervals of one standard deviation on each side of the mean.

even without age structure, but still in a continuous-time setting. It would be interesting for future research to study the implications of local risk in age-structured populations.

Expected rate of reproduction Robatto & Szentes (2017, p. 418) summarize their paper by stating that when one regarding continuous environmental variations, natural selection would ensure that people’s “choices will be based only on the expected rate of reproduction.” We interpret the expected rate of reproduction simply as the expectation of a new draw of the birth rate. In a personal communication, Balázs Szentes suggested another interpretation of the expected rate of reproduction, according to which the expected rate of reproduction should be calculated as the average birth rate of all living agents at some distant time in the future. Under this interpretation, the expected rate of reproduction induced by local risk is higher than that induced by comparable aggregate or idiosyncratic risk. From this perspective, our paper then shows that, surprisingly, the relation between the two notions of expected birth rate is more complicated than the simple one-to-one relation in Robatto & Szentes’s model, whenever the birth rate has a local (or inherited) component.

Migration between fragmented habitats Our numerical analysis suggests an important advantage to connecting isolated small habitats of an endangered species. The related existing literature (see, e.g., Burkey, 1999; Smith & Hellmann, 2002) shows that having several isolated small habitats for a species induces a larger extinction probability relative to a situation in

which the species lives in a single large habitat. This result holds in a setup in which the birth rates are decreasing in the population’s density, and are deterministic. The present paper shows that connecting isolated small habitats with immigration increases the long-run growth rate. We adopt a complementary setup of the birth rate that does not depend on the population’s density, but does have a (local) stochastic component.

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A Formal Proof

For each time t , let $w_h(t)$ be the number of agents with local birth rate x_h at time t (henceforth, x_h -agents). Let $\alpha_h(t) = \frac{w_h(t)}{w(t)}$ be the share of x_h -agents at time t . Let $\bar{b}(t)$ the average birth rate at time t : $\bar{b}(t) = \sum_k \alpha_k(t) \cdot x_k + \mu_y + z(t)$. Let $\mathbf{b}_h(t)$ be the average birth rate of x_h -agents in time t : $\mathbf{b}_h(t) = x_h + \mu_y + z(t)$. The mass of x_h -agents at time $t + \Delta t$ is given by (neglecting terms of $O((\Delta t)^2)$ in all the following equations):

$$w_h(t + \Delta t) = w_h(t) + \Delta t \cdot ((\mathbf{b}_h(t) - \delta - \lambda_x) \cdot w_h(t) + w(t) \cdot \lambda_x \cdot q),$$

where $\Delta t \cdot \mathbf{b}_h(t) \cdot w_h(t)$ is the number of offspring that have been born in this brief period to x_h -agents, $\Delta t \cdot \delta \cdot w_h(t)$ is the number of x_h -agents that have died in this brief period, $\Delta t \cdot \lambda_x \cdot w_h(t)$ is the number of x_h -agents that have changed their local birth rate in this brief period (either due to migration or due to their location having a new draw of its birth rate), and $\Delta t \cdot w(t) \cdot \lambda_x \cdot q$ is the number of agents that have changed their local birth rate and obtained a realization of x_h for their new local risk in this brief period. The mass of agents at time $t + \Delta t$ is given by

$$w(t + \Delta t) = w(t) + \Delta t \cdot (\bar{b}(t) - \delta) \cdot w(t),$$

where $\Delta t \cdot \bar{b}(t) \cdot w(t)$ is the mass of offspring born in this brief period, and $\Delta t \cdot \delta \cdot w(t)$ is the mass of agents that died in this brief period. The share of x_h -agents at time $t + \Delta t$ is given by:

$$\alpha_h(t + \Delta t) = \frac{w_h(t + \Delta t)}{w(t + \Delta t)} = \frac{\alpha_h(t) + \Delta t \cdot ((\mathbf{b}_h(t) - \delta - \lambda_x) \alpha_h(t) + \lambda_x \cdot q_x(x_h))}{1 + \Delta t \cdot (\bar{b}(t) - \delta)}.$$

Multiplying by $1 + \Delta t \cdot (\bar{b}(t) - \delta)$ and rearranging the equation gives:

$$\frac{\alpha_h(t + \Delta t) - \alpha_h(t)}{\Delta t} = (\mathbf{b}_h(t) - \delta - \lambda_x) \cdot \alpha_h(t) + \lambda_x \cdot q - (\bar{b}(t) - \delta) \cdot \alpha_h(t + \Delta t),$$

which implies, in the limit of $\Delta t \rightarrow 0$

$$\frac{d\alpha_h(t)}{dt} = (\mathbf{b}_h(t) - \delta - \lambda_x) \cdot \alpha_h(t) + \lambda_x \cdot q - (\bar{\mathbf{b}}(t) - \delta) \cdot \alpha_h(t).$$

The expression on the right-hand side simplifies to

$$\frac{d\alpha_h(t)}{dt} = (1 - \alpha_h(t)) \cdot \alpha_h(t) \cdot (x_h - x_l) + \lambda_x \cdot (q - \alpha_h(t)).$$

Let $\alpha^* \in (q, 1)$ be the unique positive number for which the right-hand side is equal to zero, where $\Delta x := x_h - x_l$:

$$\alpha^* = \frac{\Delta x - \lambda_x + \sqrt{(\Delta x - \lambda_x)^2 + 4 \cdot q \cdot \Delta x \cdot \lambda_x}}{2 \cdot \Delta x}. \quad (1)$$

It is immediate that:

$$\frac{d\alpha_h(t)}{dt} \text{ is } \begin{cases} > 0 & \alpha_h(t) < \alpha^* \\ = 0 & \alpha_h(t) = \alpha^* \\ < 0 & \alpha_h(t) > \alpha^*, \end{cases}$$

which implies global convergence to α^* from any initial state, i.e., $\lim_{t \rightarrow \infty} \alpha_h(t) = \alpha^*$. This implies that the mean birth rate converges to

$$\lim_{t \rightarrow \infty} \bar{\mathbf{b}}(t) = x_l + \alpha^* \cdot \Delta x + \mu_y + \mathbf{z}(t).$$

This, in turn, implies that the equivalent growth rate is given by:

$$g = \lim_{t \rightarrow \infty} \frac{\log \mathbf{w}(t)}{t} = \lim_{t \rightarrow \infty} (\bar{\mathbf{b}}(t) - \delta) = f(x_l, x_h, q, \lambda_x) + \mu_y + \mu_z - \delta,$$

where $f(x_l, x_h, q, \lambda_x) \equiv x_l + \alpha^* \cdot \Delta x$. The limit of $\alpha^*(\lambda_x)$ when $\lambda_x \rightarrow \infty$ is given by:

$$\begin{aligned} \lim_{\lambda_x \rightarrow \infty} \alpha^*(\lambda_x) &= \lim_{\lambda_x \rightarrow \infty} \frac{\Delta x - \lambda_x + \lambda_x \cdot \sqrt{1 + (2 \cdot q - 1) \cdot 2 \cdot \frac{\Delta x}{\lambda_x}}}{2 \cdot \Delta x} = \\ &= \lim_{\lambda_x \rightarrow \infty} \frac{\Delta x - \lambda_x + \lambda_x \cdot \left(1 + (2 \cdot q - 1) \cdot \frac{\Delta x}{\lambda_x}\right)}{2 \cdot \Delta x} = \frac{1 + (2 \cdot q - 1)}{2} = q, \end{aligned}$$

and so

$$\lim_{\lambda_x \rightarrow 0} f(x_l, x_h, q, \lambda_x) = x_l + q \cdot \Delta x = \mu_x.$$

The limit of $\alpha^*(\lambda_x)$ when $\lambda_x \rightarrow 0$ is given by:

$$\lim_{\lambda_x \rightarrow 0} \alpha^*(\lambda_x) = \frac{\Delta x + \sqrt{\Delta x^2}}{2 \cdot \Delta x} = 1,$$

and so

$$\lim_{\lambda_x \rightarrow 0} f(x_l, x_h, q_x, \lambda_x) = x_h.$$

Next, we calculate the derivative of $\alpha^*(\lambda_x)$ (1):

$$\frac{\partial \alpha^*}{\partial \lambda_x} = \frac{1}{2 \cdot \Delta x} \left(\frac{-2 \cdot (\Delta x - \lambda_x) + 4 \cdot q \cdot \Delta x}{2 \cdot \sqrt{(\Delta x - \lambda_x)^2 + 4 \cdot q \cdot \Delta x \cdot \lambda_x}} - 1 \right).$$

We have to show that $\frac{\partial \alpha^*(\lambda_x)}{\partial \lambda_x}$ is negative for any $\lambda_x > 0$. This is true iff

$$\sqrt{(\Delta x - \lambda_x)^2 + 4 \cdot q \cdot \Delta x \cdot \lambda_x} > \Delta x \cdot (2 \cdot q - 1) + \lambda_x$$

After some algebra, this condition simplifies to

$$(\Delta x)^2 \cdot (1 - (2 \cdot q - 1)^2) > 0,$$

which holds for any $q \in (0, 1)$.